

Figure 1A

1 CGGACGCGTGGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAGTGCCCCGACCGCGGCG 60
 61 CGCCGGTGCCGCGAGATGCTGGCCCAGCCGCGAGCGGCTGCTCTTCATCCTGGACGGCGCGG 120
 1 M A Q P Q R L F I L D G A D 16
 121 ACGAGCTGCCGGCGCTGGGGGGCCCCGAGCGCGCCCTGCACAGACCCCTTCGAGGCGG 180
 17 E L P A L G G P E A A P C T D P F E A A 36
 181 CGAGCGGCGCGCGGGTGTAGGCGGGCTGCTGAGTAAGGCGCTGCTGCCACGGCCCTCC 240
 37 S G A R V G G S K A L P T A L L 56
 241 TGCTGGTGACCACGCGCGCCCGCCCGGGAGGCTGCAGGGCCGCTGTGTTCCTCCCGC 300
 57 V T T R A A A P G R Q G R L C S P Q 76
 301 AGTGCGCCGAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGTATTTCTACAAGTTCT 360
 77 C A E V R G F S D K D K K K Y F Y K F F 96
 361 TCCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGTGAAGGAGAACGAGACGCTGT 420
 97 R D E R R A E R A Y R F V K E N E T F 116
 421 TCGCGCTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTGTGCACCGTGTGCGCCAGCAGC 480
 117 A C F V P F V C W I V C T V R Q Q L 136
 481 TGGAGCTCGGTGCGGACCTGTGCGGCACGTCCAAGACCACCACGTCAAGTGTACCTGCTTT 540
 137 E L G R D L S R T S K T T T S V Y L F 156
 541 TCATCACCAGCGTTCTGAGCTCGGCTCCGCTAGCCGACGGGCCCCGGTTGCAGGGCGACC 600
 157 I T S V L S S A P V A D G P R L Q G D 176
 601 TGC GCAATCTGTGCCGCTGGCCGCGAGGCGCTCCTCGGACGCGAGGGCGCAGTTTGCCG 660
 177 R N C R A R E G V L G R R A Q F A E 196
 661 AGAAGGAACTGGAGCAACTGGAGCTTCGTGGCTCCAAAGTGCAGACGCTGTTTCTCAGCA 720
 197 K E E Q L E L R G S K V Q T L F L S K 216
 721 AAAAGGAGCTGCCGGGCGTGGTGGAGACAGAGGTCACCTACCAGTTCATCGACCAGAGCT 780
 217 K E L P G V L E T E V T Y Q F I D Q S F 236
 781 TCCAGGAGTTCTCGCGGCACCTGCTACCTGCTGGAGGACGGCGGGGTGCCAGGACCG 840
 237 Q E F L A A L S Y L E D G G V P R T A 256
 841 CGGCTGGCGGCGTGGGACACTCCTGCGTGGGGACGCCAGCCGACAGCCACTTGGTGC 900
 257 A G G V G T L R G D A Q P H S H L V L 276

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Figure 1B

901	TCACCACGCGCTTCCTCTTCGGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCC	960
277	T T R F L F G Δ L S A E R M R D I E R H	296
961	ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGAC	1020
297	F G <u>C</u> M V S E R V K Q E A L R W V Q G Q	316
1021	AGGGACAGGGCTGCCCCGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGG	1080
317	G Q G C P G V A P E V T E G A K G L E D	336
1081	ACACCGAAGGCCAGAGGAGGAGGAGGAGGAGGCCCACTACCCACTGGAGTTGC	1140
337	T E E P E E E E E G E E P N Y P L E L Δ	356
1141	TGTACTGCCCTGTACGAGACGCAGGAGGACGCGTTTGTGCGCCAAGCCCTGTGCCGTTCC	1200
357	Y <u>C</u> Δ Y E T Q E D A F V R Q A L C R F P	376
1201	CGGAGCTGGCGCTGCAGCGAGTGGCGTTCTGCCGCATGGACGTGGCTGTTCTGAGCTACT	1260
377	E L A L Q R V R F C R M D V A V L S Y <u>C</u>	396
1261	GCGTGAGGTGCTGCCCTGCTGGACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTG	1320
397	V R C C P A G Q A L R Δ I S C R L V A A	416
1321	CGCAGGAGAAGAAGAAGAAGAGCCTGGGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGGCA	1380
417	Q E K K K K S Δ G K R L Q A S L G G G S	436
1381	GTTCTCAAGGCACCACAAAACAAGTCCAGCCTCCCTTCTTCATCCACTCTTTCAGGCAA	1440
437	S Q G T T K Q Δ P A S L L H P L F Q A M	456
1441	TGACTGACCCACTGTGCCATCTGAGCAGCCTCACGCTGTCCCACTGCAA ¹⁰ ACTCCCTGACG	1500
457	T D P L <u>C</u> H Δ S S L T L S H C K L P D A	476
1501	CGGTCTGCCGAGACCTTTCTGAGGCCCTGAGGGCAGCCCCGCACTGACGGAGCTGGGCC	1560
477	V C R D L S E A Δ R A A P A L T E Δ G Δ	496
1561	TCCTCCACAACAGGCTCAGTGAGGCGGGACTGCGTATGCTGAGTGAGGGCCTAGCCTGGC	1620
497	L H N R L S E A G L R M Δ S E G L A W P	516
1621	CGCAGTGCAAGGTGCAGACGGTCAGGGTACAGCTGCCTGACCCCCAGCGAGGGCTCCAGT	1680
517	Q <u>C</u> R V Q T V R V Q L P D P Q R G L Q Y	536
1681	ACCTGGTGGGTATGCTTCGGCAGAGCCCCGCCCTGACCACCTGGATCTCAGCGGCTGCC	1740
537	Δ V G M Δ R Q S P A Δ T T L D Δ S G C Q	556
1741	AACTGCCCGCCCCATGGTGACCTACCTGTGTGCAGTCCTGCAGCACCAGGGATGCGGCC	1800
557	Δ P A P M V T Y L C A V Δ Q H Q G <u>C</u> G L	576

Figure 1C

1801 TGCAGACCCCTCAGTCTGGCCTCTGTGGAGCTGAGCGAGCAGTCACTACAGGAGCTTCAGG 1860
577 Q T S A S V E S E Q S L Q E Q A 596

1861 CTGTGAAGAGAGCAAAGCCGGATCTGGTCATCACACCCAGCGCTGGACGGCCACCCAC 1920
597 V K R A K P D V I T H P A L D G H P Q 616

1921 AACCTCCCAAGGAACCTCATCTCGACCTTCTGAGGCTCTGGTGGCCAGAGCAGGGTGAAG 1980
617 P P K E L I S T F 625

1981 ACCCTAGTCAAAGTCCCTGTGGAGAGAACGGCCCATTCGAAGGGCAGGAGGATATTGCTC 2040

2041 TCGGCCTTTGGGAAACTTTTGAGCCGAGAGGCCGAGACAGGCATGTGGGAGGCCAGAC 2100

2101 ACGGCACCCTGCCCCGTCCAGGACAGGCCAGGACCTGCCCCTCTCTCCACACCTGGGGT 2160

2161 ACCCCTTCTCCCCAGCCCCACCACTACTCCACCCACCTTCCTCTCCTGAGACCCTCCAG 2220

2221 CCATTCCCCTTGAAAACACCCCCGACCCCAAGCCACAATAATGACAGCGAGAGCTCCAA 2280

2281 TTAACCTAAGCACCTACCTGGCGGCAGAATAACCCTTCACTGCCTGATCCCCATCTGCAGT 2340

2341 GTGGCCCAACAGCCCCCAGAACTATGCCACATAGACTGGAGGTAGGCAGTTCACCGTCC 2400

2401 CTCCCTGTTAGGAATGAGACCATCCCTGAGGCTATGGCCCAGGCCACAGGCGTCCAGTG 2460

2461 TCTGAGATCTTTGGGAAGGGAGACTAGGCGAGGTGGAGACAGCGCAGAACCCCCGTGCTG 2520

2521 GGTGGGAAGCATGACCACATGGTGGGTGAGCAGCCCCCATGCACTGACGGTAAATTCCTC 2580

2581 TGTGGACTCATTCTGTGTTGGTTCTATTACACCTGGCCAGGCGTGGTACAATACAGGTCG 2640

2641 GTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2689

Figure 2A

		1	50
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(1)	MAAGAWGRIACYLEFTKKEELKEFOLLANKAHSSSSSGETPAQPEKITS	
cryopyrin	(1)	-MASTRCKLARYLEDLEDVPLKKFKMHLEDYFPQKGCIPMERGCTEKADH	
Nucleotide_Binding_site	(1)	----MGFNLOALLEQLSQDELKFKYLLITTTSPAHLELQKLEHKEVUKADG	
		51	100
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(51)	MEVASYLVAQYGEORAWDLALHTWEOMGLRSLCAQAGEGAGHSPSFPQSP	
cryopyrin	(50)	VDLATIMTDFNGEEKAWAMAWWTFATNRRDLYEKAKRDEPKWGSNDARV	
Nucleotide_Binding_site	(47)	KOLWETLTTHCDSYWEMASLOMFEKMHKMDLSERAKDEVREALKSKFNK	
		101	150
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(101)	SEPHLGSPSQPTSTAVLMPWIHELPAGCTQGSERRVLRQLPDTSGRRWRE	
cryopyrin	(100)	SN-----	
Nucleotide_Binding_site	(97)	RK-----	
		151	200
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(151)	ISASHLYQALPSSPDHESPSQESPNAPTSTAVLGSWGSPPOFESLAPRQE	
cryopyrin	(102)	-----PTVTCQEDS	
Nucleotide_Binding_site	(99)	-----PLSLGITR-	
		201	250
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(201)	APGTOWPLDETSGIYYTEIREREREKSEKGPAAVVGTPFQAHSSSLCP	
cryopyrin	(111)	IEEEMWGLLEYLSRISICKMKKDYRKRYKYVRSRFQCIIDRNARLGESV	
Nucleotide_Binding_site	(107)	KERPPLDVDEMLERKTEAOKDNRCRYILKTEFEREMWKSWEFGDSKEVQV	
		251	300
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(251)	HHHPPEPSVRESLCSTWPWKNEDFNQKFTQLLLQREHPRSQDPLVKRSW	
cryopyrin	(161)	SLNKRYTRILIKEHRSQQEREQELLAIGKTKTCESEV-----	
Nucleotide_Binding_site	(157)	MAEELKMLTFFSNPR-----	
		301	350
HLRRSI1	(1)	-----	-----
caspase_recruitment_protein	(301)	PDYVEENRGHLEIRDLFGPGIDTQEPPIVVLQGAAGIGKSTLARQVKEA	
cryopyrin	(199)	-----SPKMELLFDPDDEHSEPVTVVVQGAAGIGKTLARKMMLD	
Nucleotide_Binding_site	(172)	-----VLPGPFSYTVVIYGPAGIGKTTLAGKIMLD	
		351	400
HLRRSI1	(1)	-----MLA	
caspase_recruitment_protein	(351)	WGRGOLYCDRFQHVFFVSCRELAQSKVVSLEALICGDCGATPAPITRQILS	
cryopyrin	(241)	WASGTLYQDRFDYDFYTHCREVSLVTQRSLSLILMSCCPDNPPIHKIVR	
Nucleotide_Binding_site	(202)	WAEENLIRHFKVAFVSCRELSRAGPCSAELVFRDWPELODDPHILA	
		401	450
HLRRSI1	(4)	QFORLLFILDGADELP-ALGCEEAAPCTDPFEAASCARVLGGLISKALLE	
caspase_recruitment_protein	(401)	RPRRLFLIDGVDEPCWVLQDESSELCIHWSSQPOPADALLGSLLCKTLEP	
cryopyrin	(291)	RPSRLFLMDGFDELOCADEHICPLCTDWOKMERGDIILSLIRKQLLEP	
Nucleotide_Binding_site	(251)	QARKLLEVTIDGFDELGAAPGALIEPCGDWEKKKVPVILLGSLINRVMLEP	
		451	500
HLRRSI1	(53)	TALLVTTRAAAPGRLOGRLCSPOCAEVRGFSDEKKEYFYKTERDERRA	
caspase_recruitment_protein	(451)	EASLLIPARITATONLIPSLQARWVEVLGFSESEKKEYFYRYFTDERQA	
cryopyrin	(341)	EASLLITTRPVALEKLOHLLDHPRVEILGFSEAKRKEYFYRYFSDEAQA	
Nucleotide_Binding_site	(301)	KAALLVTTRPRALRDLRILAEPIYTRVEGLEEDKRAYELRFEDELOA	
		501	550
HLRRSI1	(103)	ERAPREVKEKETLFAICEVPEVCWIVCTVLRQCELCRDLSRTSKTTTSV	
caspase_recruitment_protein	(501)	IRAFRLVRSNKELWALCLVPPVSWLACTCLMOQMKRKERTILTSKTTTTL	
cryopyrin	(391)	RAEFLIQENEVLFTMCFELVCWIVCTGLKQOMESGKSLAQTSKTTTAV	
Nucleotide_Binding_site	(351)	MRAFLMRSNAALFOLGSAPAVCWIVCTTLLLOMENGEDVPPTLLRTSL	
		551	600
HLRRSI1	(153)	YLLFITSVLSSAEVADCPRLQCDLRNLCLRLAREGLCRRAQFAEKHLGQI	
caspase_recruitment_protein	(551)	CHHYLQALCAQF-----LGPOLRDLCSLAAEGIWCKKELFSPEDLRKH	
cryopyrin	(441)	YVFFLSLILQPRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNH	
Nucleotide_Binding_site	(401)	LRFLQSRNP-----QCAQLRCALRITSLSLAAGCWAQNSWHRDLERL	

Figure 2B

		601		650
HLRRS11	(203)	ELRGSKVCTFLFLSKKE	PGVLETEEMTYCFIDCSFOEFLAAMSYLLED	GGV
caspase_recruitment_protein	(595)	GLDGAITSTFLKMG	---LLOEHPIPLSYSFHLCFOEETFAAMSYWLEDEK	
cryopyrin	(491)	GLQKADVSAFLRMN	LFQNEVDCEKFSYFIHMTFOEETFAAMYLLLEKEKE	
Nucleotide_Binding_site	(446)	GVQESDRLRLFLQGD	---LFRQDRVSEGCYSFIHLSFOEETFAAFYTLLEKEE	
		651		700
HLRRS11	(253)	PRTAAGC	-----VGTLLRCDAOPHSH	VLTTTRFLFGLLSAERMRI
caspase_recruitment_protein	(642)	-----	GRGKHSNCIIDEKTE	LAAYGHHGLFGASTTRFLFGLLSEGERE
cryopyrin	(540)	GRINVP	CSRKLPSRDVTVLL	ENYGRKEKGLTFVVRFLFGLVNCERTSY
Nucleotide_Binding_site	(495)	EDRDGHTWDIG	---DVQKLLSGVERLRNP	ELIQAGYYSFGIANERKARE
		701		750
HLRRS11	(293)	LEERHFGMYSERV	KQELRWVQGGQCGPGVAPEVTEGAKGL	LEETPEE
caspase_recruitment_protein	(686)	MENLHCHRFSC	---CRNLMONVPSL	-----QLLLQPHS
cryopyrin	(590)	LEKRLSCHRFSC	RLLELLKWIIVK	-----AKAKKLQIQESC
Nucleotide_Binding_site	(541)	LEATFGCRMSPD	IKQELLRCDISC	-----KCGHSTWTDLO
		751		800
HLRRS11	(343)	EEEGEEPNY	LELLYCLYETOE	DAFVRCAICREPEELRLRVRFRCMDVAV
caspase_recruitment_protein	(716)	-----	LESILHLYETRNKTF	LTQMAHFEEMCMC
cryopyrin	(626)	-----	LELLYCLYEMQED	DFVQRANDVFPATL
Nucleotide_Binding_site	(576)	-----	ELLGOLVESQEEELV	KEMMACKEISL
		801		850
HLRRS11	(393)	LSYCVRC	PAGCALRLSCRLVAACEKKKKS	LCRLQASLGGSSQ
caspase_recruitment_protein	(754)	CTECHKFSRHVK	LQLLEGQHRSTWSPSMVLFRWVPVTDAYWQLLS	
cryopyrin	(664)	SSFCIENCHRVES	LSLIGLHMPKEEEEEKE	GRHLDLVQCPLPSSSHAA
Nucleotide_Binding_site	(612)	SSFCYKHCHRN	LQKMSIQVIKENL	PEENVTASESBAEYVRSODBOHMPFWT
		851		900
HLRRS11	(439)	-----	-----	-----
caspase_recruitment_protein	(803)	-----	-----	-----
cryopyrin	(714)	CSHGIVNSH	-----	---LT
Nucleotide_Binding_site	(662)	DLCSIFG	SNKDLMLAINDSFLSASLVRI	LCEQIASDTHLQRVVFKNLS
		901		950
HLRRS11	(439)	-----	---CTTKCLPAST	LEELFQAMTEELCHSSLT
caspase_recruitment_protein	(803)	-----	---VIKVTRNLKELDLS	SGNSLSHSAVKSCLCTLRNPRCLLETLR
cryopyrin	(725)	SSFCRGLFSVL	STSSQSLTELDLSDNSL	GDGMRVLCETLQHEGCGNIRRLW
Nucleotide_Binding_site	(712)	PADAHRNLCL	ALRGHKTVTYLTLC	QNDQDDMEFPALCEVLRHEECNRLRYLG
		951		1000
HLRRS11	(468)	LSHCKLPDAV	CRDLSEALRAAPALTELGLLHNR	LSAGLEMISEGAWEQ
caspase_recruitment_protein	(844)	LACGLTAD	DCDLAEGLRANCTITELDLS	FNVLDAKALHCQRLEOPS
cryopyrin	(775)	LRCGLSH	ECCFHSLSVSSNQKLVELDLS	SDNALGDFGIELLCVGLKHL
Nucleotide_Binding_site	(762)	LVS	CSATTQQWADLSLAEVNC	SLTCVNLSDNELIDEGARLLYTTTRHPK
		1001		1050
HLRRS11	(518)	CRVCTVRV	QLPDPQ-RGLCYLVCM	LROSPALTITDLSGCCLPAPMVITLC
caspase_recruitment_protein	(894)	CKLQRLQ	LVSCGLTSDCCODLASVLS	ASPSLKELDLQNNLDVGVRLIC
cryopyrin	(825)	CNLRKLWL	VSCCLTSACCDLASVLST	SHSLTRLYVGENALGDSGVAILC
Nucleotide_Binding_site	(812)	CFLQRLS	LENCHLTENCRDLAEVLVVS	RELTHLCLAKNPENGTGVRELIC
		1051		1100
HLRRS11	(567)	AVLCHQCC	GLOTLGLASVLESEQSLQEL	QAVKRAKPLVITTHIPALDGHQP
caspase_recruitment_protein	(944)	EGLRHPACK	LIRLGLDOTTLSDEMROEL	RADEOEKEPOLLISSRKPSVMT
cryopyrin	(875)	EKARNFOCN	LQKGLVNSGLTSVCCSAL	SSYSTNQNITHLIRGNITLCD
Nucleotide_Binding_site	(862)	EGLRYPECK	LQTLVFWNCDTITS	EGCCETLKKLQEKSSILCLDGLNHEIGV
		1101		1150
HLRRS11	(617)	EPKEL	ESTF	-----
caspase_recruitment_protein	(994)	PIEGIDT	GEMSNSTSSLRQR	LGSERAASHVAQANLKLLDVSRIPIAE
cryopyrin	(925)	KGKILLCE	GLLHEDCKLOVLELDN	CNTTSHCCWDISILLTSSOSLRKLSL
Nucleotide_Binding_site	(912)	KGKELCE	ALRRKLCNTRCLW	WGCSFPRES
		1151		1200
HLRRS11	(626)	-----	-----	-----
caspase_recruitment_protein	(1044)	AGSSP	VVPVETLCVPSPAS	CDLHTKPLGTDDEFGPTGPVATEVWDK
cryopyrin	(975)	CNN	---DLCDTGVMECEVLR	KQSCCLQNLGSEMMFNYEYKSALETLCE
Nucleotide_Binding_site	(961)	CNN	---PLGSSGVKMF	ETTLICSSGTETLRKIDNDELNKLLEETFE

Figure 2C

		1201	1250
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1094)	EKNLYRVHFPVAGSRRWPNTGLCHVVREAVTVEIEFCVWDQFLGEINPQH	
cryopyrin	(1022)	EKPEDLTIVVEPSW	
Nucleotide_Binding_site	(1008)	KNPCHITDTEKHHHPNAERPSSHDEMT	
		1251	1300
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1144)	SWMVAGPLLDIKAEPGAVEAVHLPHFVALQGGHVDTSIFQVAHFKEEGML	
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1301	1350
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1194)	LEKPARVELHHIVLENPSFSPLGVLLKMIHNALRFIPVTSVLLYHRLHP	
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1351	1400
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK	
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1401	1450
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1294)	DKKDETLVWEALVKPGDLMPATTLIPPACIAVPSPLDAPQLLHFVDQYRE	
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1451	1500
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1344)	QLIARVTSVEVVLDKLHGQVLSQEQYERVLAENTRPSQMRKLFSLSQSWD	
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1501	1536
HLRRS11	(626)	-----	-----
caspase_recruitment_protein	(1394)	RKCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS	
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----

Figure 3

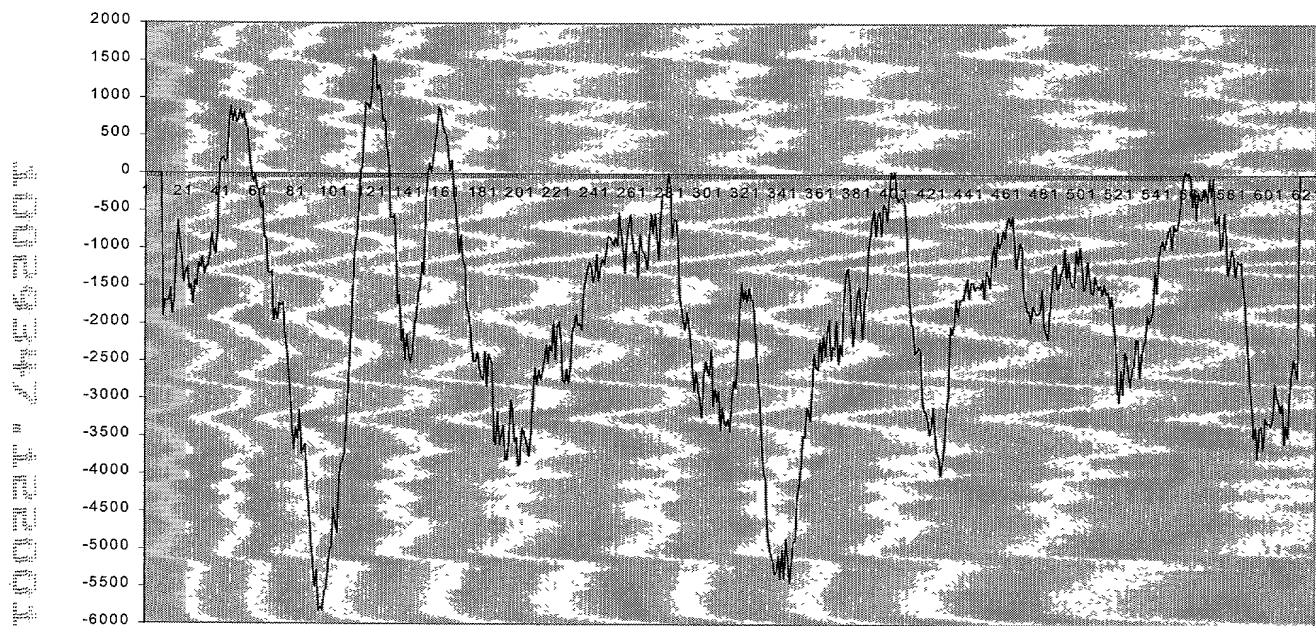


Figure 4

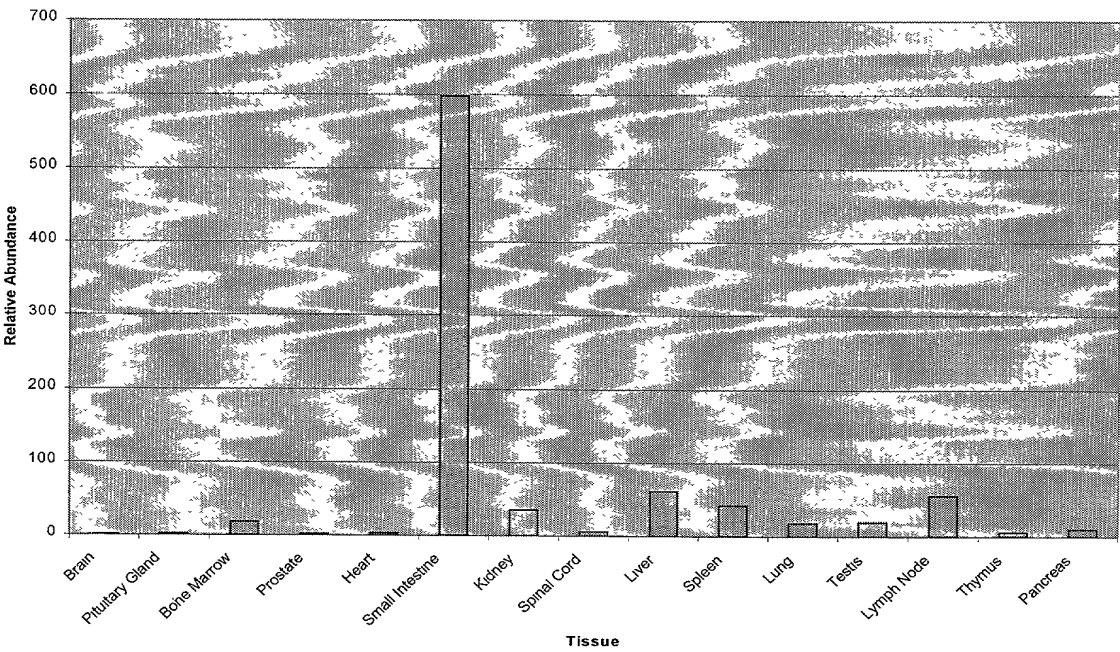


Figure 5.

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%